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PATENT COOPERATION TREATY

PCT

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INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 126690.7 DAB	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/IL 00/ 00427	International filing date (day-month-year) 19/07/2000	(Earliest) Priority Date (day-month-year) 20/07/1999
Applicant COMPUGEN LTD. et al.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 3 sheets.

☒ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

- a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

- b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :

☒ contained in the international application in written form.

☒ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☐ furnished subsequently to this Authority in computer readable form.

☐ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☐ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☐ **Certain claims were found unsearchable** (See Box I).

3. ☐ **Unity of invention is lacking** (see Box II).

4. With regard to the **title**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No.

☒ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

2

☐ None of the figures.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IL 00/00427

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C07K16/28 A61K38/17 A61K39/395
A61K48/00 C12Q1/68 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, STRAND, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! EMBL; ID HS884118; AC R49884, 24 May 1995 (1995-05-24) HILLIER L ETAL: "CD40L receptor precursor" XP002155584 EST nucleotide sequence ---	2,7,8
X	DATABASE EMBL 'Online! EMBL; ID AI784157; AC AI784157, 2 July 1999 (1999-07-02) NATIONAL CANCER INSTITUTE, CANCER GENOM ANATOMY PROJECT (CGAP): "CD40L receptor precursor" XP002155585 EST nucleotide sequence ---	2,7,8

-/--



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *S* document member of the same patent family

Date of the actual completion of the international search

15 December 2000

Date of mailing of the international search report

28/12/2000

Name and mailing address of the ISA

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Authorized officer

Espen, J

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IL 00/00427

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of the relevant passages	Relevant to claim No
X	<p>DATABASE EMBL 'Online! EMBL; ID HSH94398; AC H94398, 6 December 1995 (1995-12-06) HILLIER L ET AL: "CD40L receptor precursor" XP002155586 EST nucleotide sequence ---</p>	1,7,8
X	<p>DATABASE GCG_GENESEQ:D 'Online! GCG; ID V64740; AC V64740, 29 January 1999 (1999-01-29) CAPON D ET AL: "Human immunodeficiency virus" XP002155587 HIV anti-viral oligonucleotide primer ---</p>	2,7,8
X	<p>DATABASE EMBL 'Online! EMBL; ID MMA60117; AC AA060117, 24 September 1996 (1996-09-24) MARRA M ET AL: "Mouse murine CD40 mRNA" XP002155588 EST nucleotide sequence ---</p>	1,7,8
X	<p>EP 0 555 880 A (DARTMOUTH COLLEGE ;GEN HOSPITAL CORP (US); SQUIBB BRISTOL MYERS CO) 18 August 1993 (1993-08-18) column 7 -column 9; figure 8A column 18 -column 19 ---</p>	1,3,5-9, 22
X	<p>WO 98 53842 A (UNIV PENNSYLVANIA) 3 December 1998 (1998-12-03) figure 1 ---</p>	3
X	<p>WO 97 23614 A (AMGEN INC ;LACEY DAVID L (US); BOYLE WILLIAM J (US); CALZONE FRANK) 3 July 1997 (1997-07-03) figure 2D figure 2E SEQ ID NO 132 -----</p>	3

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IL 00/00427

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
EP 0555880	A	18-08-1993	AU 3298893 A	19-08-1993
			AU 701306 B	28-01-1999
			AU 7198096 A	06-02-1997
			CA 2089229 A	15-08-1993
			FI 930605 A	15-08-1993
			JP 6220096 A	09-08-1994
			NO 930521 A	16-08-1993
			NZ 245898 A	27-04-1995
			ZA 9301013 A	20-09-1993
WO 9853842	A	03-12-1998	AU 7603698 A	30-12-1998
			EP 1011704 A	28-06-2000
WO 9723614	A	03-07-1997	AU 710587 B	23-09-1999
			AU 1468697 A	17-07-1997
			BG 101813 A	30-09-1998
			CA 2210467 A	03-07-1997
			CN 1182452 A	20-05-1998
			CZ 9702538 A	17-03-1999
			DE 19654610 A	26-06-1997
			EP 0784093 A	16-07-1997
			EP 0870023 A	14-10-1998
			FR 2742767 A	27-06-1997
			GB 2312899 A, B	12-11-1997
			HU 9801122 A	28-08-1998
			JP 11503616 T	30-03-1999
			NO 973699 A	21-10-1997
			NZ 326579 A	28-01-1999
			PL 321938 A	05-01-1998
			SK 110797 A	12-07-1999
			TR 970550 A	21-07-1997
			US 6015938 A	18-01-2000

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 126690.7 DAB	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/IL00/00427	International filing date (<i>day/month/year</i>) 19/07/2000	Priority date (<i>day/month/year</i>) 20/07/1999
International Patent Classification (IPC) or national classification and IPC C12N15/12		
Applicant COMPUGEN LTD. et al.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2. This REPORT consists of a total of 10 sheets, including this cover sheet.

☒ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of 4 sheets.

3. This report contains indications relating to the following items:

I ☒ Basis of the report

II ☐ Priority

III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

IV ☐ Lack of unity of invention

V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

VI ☐ Certain documents cited

VII ☐ Certain defects in the international application

VIII ☒ Certain observations on the international application

Date of submission of the demand 18/02/2001	Date of completion of this report 01.11.2001
Name and mailing address of the international preliminary examining authority: <div style="display: flex; align-items: center;"> <div> European Patent Office - P.B. 5818 Patentlaan 2 NL-2280 HV Rijswijk - Pays Bas Tel. +31 70 340 - 2040 Tx: 31 651 epo nl Fax: +31 70 340 - 3016 </div> </div>	Authorized officer Schmitz, T Telephone No. +31 70 340 4494



INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/IL00/00427

I. Basis of the report

1. With regard to the **elements** of the international application (*Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17)*):

Description, pages:

1-27,29-41	as originally filed			
28	as received on	02/08/2001	with letter of	26/07/2001

Claims, No.:

11-16	as originally filed			
1-10,17-25	as received on	02/08/2001	with letter of	26/07/2001

Claims, pages:

42,44,45	as received on	02/08/2001	with letter of	26/07/2001
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Drawings, sheets:

1/12-12/12	as originally filed			
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Sequence listing part of the description, pages:

1-9, as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☒ contained in the international application in written form.
- ☒ filed together with the international application in computer readable form.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/IL00/00427

- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:
- ☐ the drawings, sheets:

5. ☒ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

see separate sheet

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

- ☐ the entire international application.
- ☒ claims Nos. 10-14.

because:

- ☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):
- ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):
- ☒ the claims, or said claims Nos. 10-14 are so inadequately supported by the description that no meaningful opinion could be formed.
- ☐ no international search report has been established for the said claims Nos. .

2. A meaningful international preliminary examination cannot be carried out due to the failure of the nucleotide

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/IL00/00427

and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

- ☐ the written form has not been furnished or does not comply with the standard.
- ☐ the computer readable form has not been furnished or does not comply with the standard.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Yes:	Claims	1, 2, 4, 8, 15-25
	No:	Claims	3, 5-7, 9
Inventive step (IS)	Yes:	Claims	1, 2, 4, 8, 15-21
	No:	Claims	3, 5-7, 9, 22-25
Industrial applicability (IA)	Yes:	Claims	1-9, 15-25
	No:	Claims	-

2. Citations and explanations **see separate sheet**

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:

see separate sheet

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/IL00/00427

Re Item I

Basis of the report

1. New claim 6 of the application refers to "a purified antibody which binds specifically to an amino acid sequence present in any of the amino acid sequence of claim 3 or 4 and not present in the native CD40R". Since it is not clear what the sequence of the native CD40R is, the claim lacks clarity and does not meet the requirements of Article 6 PCT. Furthermore, the application lacks support for the restriction to "(...) amino acid sequences of claim 3 or 4 and not present in the native CD40R." The international preliminary examination report will therefore be based on the originally filed claim 6 (Article 34(2)(b) and Rule 70.2(c) PCT).
2. This preliminary examination report is based on the sequence listing as originally filed.
According to the applicant, the sequence listing was changed to indicate that the sequences are of mouse origin. However, no amended sequence listing was received. Furthermore, the application does not provide a basis for this amendment (Article 34(2)(b) and Rule 70.2(c) PCT).

Re Item III

Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

3. According to the applicant, all claimed sequences are of mouse origin. Claims 10-14 lack support from the description in so far as it is not clear how an antibody against a mouse epitope can be used in a pharmaceutical composition which is obviously aimed at treating human diseases. Therefore, these (purely speculative) claims do not meet the requirements of Article 6 PCT.

Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

Reference is made to the following document:

D1: EP-A-0 555 880 (DARTMOUTH COLLEGE ;GEN HOSPITAL CORP (US);
SQUIBB BRISTOL MYERS CO) 18 August 1993 (1993-08-18)

4. Claim 1 of the present application refers to an isolated nucleic acid sequence of an alternative splicing variant of CD40 receptor (CD40R), selected from
- a) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to 6; or
 - b) nucleic acid sequences having at least 90% identity with any one of the sequences of a) over the entire length of the sequence.

The document D1, which is considered to represent the closest prior art, discloses a nucleic acid sequence coding for a CD40 receptor having less than 90% identity with the sequences of claim 1.

The problem to be solved may therefore be regarded as the provision of nucleic acid sequences coding for splice variants of the CD40 receptor.

The solution proposed, namely the provision of SEQ ID NO: 1-6 is non-obvious in view of the prior art and therefore involves an inventive step.

Therefore, the subject matter of claim 1 is new and inventive.

Furthermore, the provision of nucleic acid sequences complementary to said sequences and their ligation into an expression vector is also new and inventive.

In conclusion, the subject matter of claims 1, 2 and 8 meets the requirements of Article 33(2) and (3).

5. Claim 4 of the present application refers to amino acid sequences for CD40R splice variants.

The document D1, which is considered to represent the closest state of the art, discloses an amino acid sequence having 93.7% identity in a 143 amino acid overlap with SEQ ID NO 7 (160 aa) of the present application, and 88.1% identity in a 277 amino acid overlap with SEQ ID NO 8.

The problem to be solved may therefore be regarded as the provision of amino acid sequences of splice variants of the CD40 receptor.

The solution proposed, namely the provision of SEQ ID NO: 7-12 is non-obvious in view of the prior art and therefore involves an inventive step.

In conclusion, the subject matter of claim 4 is new and inventive and meets the requirements of Article 33(2) and (3).

6. Claims 15-20 refer to a method for detecting the presence, determining the level and determining the ratio of the nucleic acids of claims 1 or 2 (including their transcripts) respectively.

Claim 21 refers to a method for identifying candidate compounds capable of binding to the amino acid sequences of the present application.

Prior art does not disclose any of these methods in conjunction of the nucleic acids of claim 1 or 2 (including transcripts).

Therefore, claims 15-21 meet the requirements of Articles 33(2) and (3) PCT.

7. The present application does not meet the requirements of Article 33(2) for the following reasons:

The document D1 discloses (the references in parenthesis applying to this document) a 1004 bp long nucleic acid sequence coding for CD40 together with

the corresponding amino acid sequence (depicted in Fig 8A), being a homologue of the CD40R splice variants of the present application.

The same document (Figure 8B) further discloses an expression vector comprising DNA coding for the extracellular part of CD40. This vector was transfected into COS cells (column 15, line 26 to line 29).

Document D1 (column 6, line 46 to line 52) also discloses a monoclonal antibody (G28-5, produced by the hybridoma having accession number HB9110, deposited with the American Type Culture Collection) directed against CD40.

Furthermore, Claim 21 of document D1 discloses a pharmaceutical composition comprising CD40-Ig in a suitable pharmaceutical carrier.

In view of document D1, the following should be noted:

- a) Claims 3 and 5 of the present application are not new, because the amino acid sequence depicted together with the coding DNA in document D1, Figure 8A is considered as a homologue of the sequences SEQ ID No 7 and 8 of the present application, because of the high degree of identity:

The disclosed amino acid sequence has a 93.7% identity in a 143 amino acid overlap with SEQ ID NO 7 (160 aa) of the present application, and 88.1% identity in a 277 amino acid overlap with SEQ ID NO 8.

- b) The subject matter of claim 6 lacks novelty because it can be assumed with certainty that the disclosed antibody will also bind to the splice variants of the present application.
- c) The subject matter of claim 7 lacks novelty because an expression vector comprising any of the nucleic acid sequences of claim 1 or 5 is known.
- d) A host cell (claim 9) transfected with the expression vector of claim 7 is not new.

In conclusion of the paragraphs above, the subject matter of claims 3, 5-7 and 9 is not new and does not meet the requirements of Article 33(2) PCT.

8. Claims 22-25 of the present application refer back to the homologues of claim 3 and the antibody of claim 6, which are disclosed in the prior art (see above). The subject-matter of claims 22-25 does not involve an inventive step for the following reasons:
- a) Document D1 (column 6, line 46 to line 52), which is considered to represent the closest prior art, discloses a monoclonal antibody (G28-5) directed against CD40. This antibody was used for the detection of a CD40 fusion protein in a biological sample by flow cytometry (D1, column 10, lines 24-40). It can be assumed with certainty that this antibody will also bind to the splice variants of the present application.
- The subject-matter of claims 22-24 differs from the disclosure in D1 in that the antibody of the present application is used for detecting the level and the ratio of a specific amino acid sequence, such as the splice variants of CD40R of the present application.
- The problem to be solved by the present application may therefore be regarded as providing a method for the detection of the level and the ratio of CD40R splice variants in a biological sample.
- The solution proposed in claims 22-24 of the present application cannot be considered as involving an inventive step, because the skilled person would regard it as a normal procedure to use the known antibody in the methods set out in claims 22 and 23.
- b) In view of paragraph a) above, the normalisation of the amount of an antibody-antigen complex as claimed in claim 23(b) of the present application does not add technical features that would render this part of the application inventive.

- c) Furthermore, in view of paragraph a) above, a method for the detection of the ratio between the level of two amino acids in a biological sample, wherein the first and the second sample are the same sample does not add technical features that would render this part of the application inventive.

In conclusion of paragraphs a)-c) above, the subject-matter of claims 22-25 does not involve an inventive step and does not satisfy the criterion set forth in Article 33(3) PCT.

Re Item VIII

Certain observations on the international application

9. The description refers to some of the SEQ ID NOs as being of human origin and to some as being of mouse origin (e.g. page 4, lines 3 and 4).

According to the applicant, the sequence listing should refer to the sequences as being of mouse origin, instead of human (as originally filed). However, no amended sequence listing was filed in the procedure.

Assuming that all sequences are of mouse origin, it does not appear logical to refer to the mouse sequences of the present application as alternative splice variants of the human CD40 receptor (page 3, lines 20-26 of the present application).

Therefore, the present application lacks clarity and does not meet the requirements of Article 6 PCT.

Apart from the clarity issue above, it does at present not appear possible to amend the sequence listing in view of Article 34(2)(b) and Rule 70.2(c) PCT.

protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

C. Use of variant to produce proteins

5 C.1 Separation:

Sf-9 cells were infected with sCD40 (soluble CD40) expressing baculovirus (Ac-sCD40) comprising the nucleic acid sequence of SEQ ID NO:3 at MOI of 2. The cells were grown in 28°C at continuous shaking (90rpm). At 60 hours post infection (hpi) the medium was collected and cells were separated
10 from the medium by centrifugation at 5000RPM for 5 minutes. 10ml medium was separated using cation exchange chromatography with SP-Sepharose column. The Column was equilibrated with PBS pH-6.5 and following loading of the sample on the column the column was washed with PBS to elute the unbound proteins (flow through fraction). Elution was done with increasing concentration
15 of NaCl at flow rate of 2ml/min (5%NaCl/min).

The different fractions were subjected to SDS-PAGE electrophoresis and to western blotting using anti mCD40 antibody, and the results are shown in Fig. 2.

20 C.1 Secretion:

Sf-9 cells were infected with sCD40 expressing baculovirus (Ac-sCD40) at MOI of 2. The cells were grown at 28°C at continuous shaking (90rpm) and 1ml samples were collected at 24, 48 and 60 hours post infection (hpi). Following centrifugation Cells pellet was lysed with lysis buffer (50mM Tris pH
25 7.5, 1% triton X100, and protease inhibitor cocktail) at 4°C for 30 min and sonicated for 30 seconds. The sample was centrifuged for 10 minutes at 14000rpm and the sup was designated Pellet. 40 µl of the pellet preparation and of the medium (Designated Medium) were supplemented with sample buffer and electrophoreses on a 15% SDS-PAGE. Following electrophoresis the gel was
30 subjected to a semi dry protein transfer onto a nitrocellulose membrane. The

02.08.2001

CLAIMS:

(78)

1. An isolated nucleic acid sequence, of an alternative splicing variant of CD40 receptor (CD40R), selected from:
 - (i) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to SEQ ID NO: 6; or
 - (ii) nucleic acid sequences having at least 90% identity with any one of the sequences of (i) over the entire length of the sequence.
2. An isolated nucleic acid sequence complementary to the nucleic acid sequence of Claim 1.
3. An amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence coded by the isolated nucleic acid sequence of Claim 1; and
 - (ii) homologues of the amino acid sequences of (i) in which one or more amino acids has been added, deleted, replaced or chemically modified.
4. An amino acid sequence according to Claim 3, as depicted in any one of SEQ ID NO:7 to SEQ ID NO:12.
5. An isolated nucleic acid sequence coding for any one of the amino acid sequences of Claim 3 or 4.
6. A purified antibody which binds specifically to an amino acid sequence present in any of the amino acid sequence of Claim 3 or 4 and not present in native CD40R.
7. An expression vector comprising any one of the nucleic acid sequences of Claim 1 or 5 and control elements for the expression of the nucleic acid sequence in a suitable host.
8. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.
9. A host cell transfected by the expression vector of Claim 7 or 8.
10. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:

17. A method for determining the ratio between the level of the nucleic acid sequence of a CD40R variant in a first biological sample and the level of the original CD40R sequence from which the variant has been varied by alternative splicing, in a second biological sample comprising:

- (a) determining the level of the CD40R variant nucleic acid sequence in the first biological sample according to the method of Claim 16;
- (b) determining the level of the CD40R original sequence in the second biological sample; and
- (c) comparing the levels obtained in (a) and (b) to give said ratio.

18. A method according to Claim 17, wherein said first and said second biological samples are the same sample.

19. A method according to any of Claims 15 to 18, wherein the nucleic acid material of said biological sample are mRNA transcripts.

20. A method according to Claim 19, where the nucleic acid sequence is present in a nucleic acid chip.

21. A method for identifying candidate compounds capable of binding to the amino acid sequence of Claim 3 or 4 and affecting the binding affinity of said sequences to at least one ligand of CD40, the method comprising:

- (i) providing any one of the amino acid sequences as defined in Claim 3 or 4;
- (ii) contacting a candidate compound with said amino acid sequence in the presence of at least one ligand of CD40;
- (iii) determining the effect of said candidate compound on the binding of said amino acid to said ligand and selecting those compounds which show a significant effect on said binding.

22. A method for detecting any one of the amino acid sequences of Claim 3 or 4 in a biological sample, comprising:

- (a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and
- (b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.

23. A method for detecting the level of the amino acid sequence of any one of Claim 3 or 4 in a biological sample, comprising:

(a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and

(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

24. A method for determining the ratio between the level of any one of the amino acid sequences of Claims 3 or 4 of variant CD40R present in a first biological sample and the level of the original CD40R amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

(a) determining the level of the amino acid sequences of Claims 3 or 4 into a first sample by the method of Claim 23;

(b) determining the level of the original CD40R amino acid sequence in the second sample; and

(c) comparing the level obtained in (a) and (b) to give said ratio.

25. A method according to Claim 24, wherein said first and said second biological samples are the same sample.

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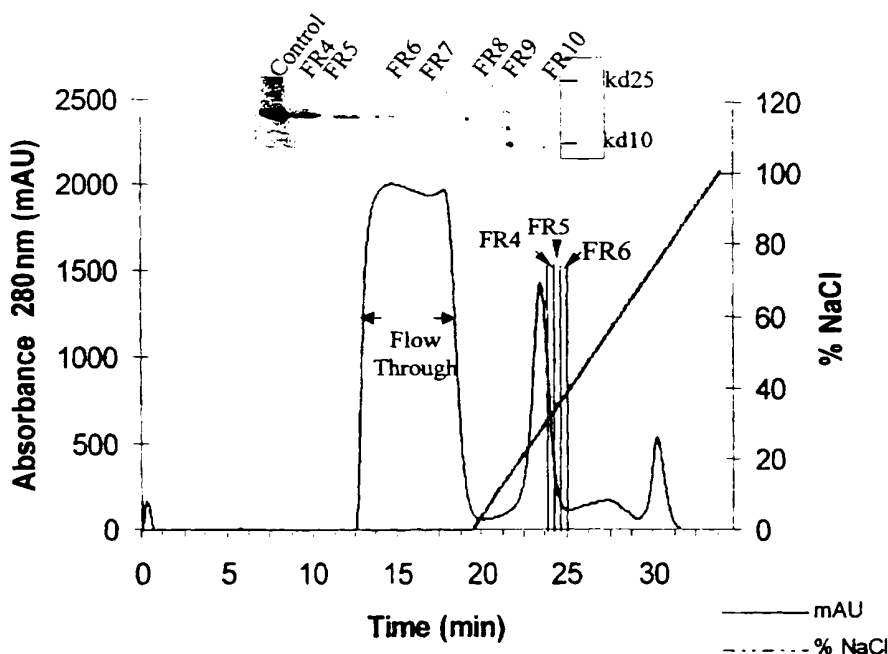
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(54) Title: SPLICE VARIANTS OF CD40-RECEPTOR



(57) Abstract: The present invention concerns six novel variants of alternative splicing of the CD40 receptor.

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SPLICE VARIANTS OF CD40-RECEPTOR

FIELD OF THE INVENTION

The present invention concerns novel nucleic acid sequences, vectors and host cells containing them, amino acid sequences encoded by said sequences, and antibodies reactive with said amino acid sequences, as well as pharmaceutical
5 compositions comprising any of the above. The present invention further concerns methods for detecting nucleic acid and amino acid sequences in a sample.

BACKGROUND OF THE INVENTION

CD40 is a cell surface receptor, which belongs to the TNF-R family, and which was first identified and functionally characterized on B lymphocytes.
10 However, in recent years it has become clear that CD40 is more widely expressed, including expression on monocytes, dendritic cells, endothelial cells and epithelial cells. Therefore it is now thought that CD40 plays a more general role in immune regulation.

The CD40 protein is a 45-50 kDa glycoprotein of 277 AA, the 193 AA
15 extracellular domain is composed of four imperfect repeats of about 40 residues, anchored by a superimposable pattern of six cysteines. This organization is found in the other members of the TNF-R family.

CD40 is expressed by multiple cell types. In the hematopoietic system, it is expressed on CD45⁺ hematopoietic progenitors, B cell progenitors, mature B
20 lymphocytes, plasma cells, monocytes, dendritic cells, eosinophils, basophils and on some T lymphocytes. CD40 is also expressed on non-hematopoietic cells such as endothelial cells, fibroblasts and epithelial cells.

Expression cloning using a CD40-Fc fusion protein allowed the isolation of a CD40-ligand (CD40-L) from activated T cells. The human CD40-L is a polypeptide of 261 AA including a 215 AA extracellular domain with five cysteines. CD40-L is a member of the Tumor Necrosis Factor family.

5 CD40-R bound to its ligand activates protein-tyrosine kinases, including *Lyn* and *Syk* and induces the tyrosine phosphorylation of multiple substrates including phosphatidylinositol 3-kinase and phospholipase $C\gamma 2$.

CD40 also interacts with TRAF3 protein (TNF-R Associated Factor-3), also identified under the name CRAF1, CD40bp, LAP1 and CAP1 (18-21).
10 TRAF3 is a 62 kD intracellular protein which is expressed in almost all cell types. The protein contains several functional domains which might be involved in signal transduction.

In addition, CD40 has been demonstrated to associate with TRAF2, a molecule which also associates with TNF-R2. The induction of NF- κ B activation
15 via CD40 cross-linking (and also via TNF-R2) could be attributed to TRAF2 signaling.

CD40 ligation activates resting B cells as shown by increase in size and expression of new surface molecules involved in homotypic and heterotypic aggregation (CD23, VLA-4), as well as T cell costimulation (CD80/CD86).
20 Furthermore, CD40-activated B cells secrete a panel of cytokines which may act as autocrine and paracrine growth and differentiation factors.

CD40 is further known to be expressed on professional antigen presenting cells such as monocytes and dendritic cells, and its ligation to the above cells results in secretion of multiple proteins including cytokines such as IL1, IL5, IL8
25 IL10, IL12, TNF α , MiP1 α , as well as enzymes such as matrix metalloproteinase (MMP).

The importance of this receptor-ligand pair for the cellular immune response, has been demonstrated by the diminished immunity against several pathogens in CD40 and CD40-L knockout mice. In keeping with this, CD40
30 ligation turns on monocyte tumoricidal activity as well as NO synthesis.

- 3 -

Administration of antibodies to CD40-L has been shown to prevent the establishment of autoimmune symptoms in various murine models including: (1) collagen type II-induced arthritis: a model for human rheumatoid arthritis; (2) lupus nephritis in lupus prone mice that represent models for the systemic lupus erythematosus; (3) protcolipoprotein induced experimental encephalomyelitis: a model of human multiple sclerosis.

Administration of anti-CD40-L antibodies further has been demonstrated to prevent the development of graft versus host disease (GVHD) that occurs as a major complication of allogeneic bone marrow transplantation (van Kooten, C. and Banachereau, J., *Frontiers in Bioscience*, d1-11 January 1, (1997)).

GLOSSARY

In the following description and claims use will be made, at times, with a variety of terms, and the meaning of such terms as they should be construed in accordance with the invention is as follows:

“CD40R Variants nucleic acid sequences” – the sequence shown in any one of SEQ ID NO: 1 to SEQ ID NO: 6 sequences having at least 90% identity (see below) to said sequences and *fragments* (see below) of the above sequences of least 20 b.p. long. These sequences are sequences coding for a novel, naturally occurring, alternative splice variants of the native and known CD40R, depicted in the Swiss Prot as CD40_HUMAN under Accession Number P25942 which is the sequence coding for the human 45-50 kDa glycoprotein of 277 amino acid. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of the CD40R gene and not merely truncated, mutated or fragmented form of the gene.

The description of the CD40R variants and their difference from the original sequence is summarized in Table 1 as follows:

Table 1

SEQ ID NO:	New variant internal name	Length (amino acids)	Description of the variation (comparing to the original sequences)
1		160	Has the extracellular domain of the native CD40 gene from signal peptide up to the position of the amino acid before the transmembrane region.
2		246	Has the extracellular domain of the native CD40 gene from signal peptide up to the position of the amino acid before the transmembrane region.
3	Mcd40-pFB1-1-5	156	Contains 135 N-terminal amino acids, including entire TNFR-Cys repeats 1 and 2, and part of the TNFR-Cys repeat 3. Alternative 21 amino acids at the C terminus. Missing the TNFR-Cys repeat #4, part of the TNFR-Cys repeat #3, the TM domain and the cytoplasmic domain.
4	MCD40Alt8	203	Contains 165 N-terminal amino acids, including entire TNFR-Cys repeats 1, 2, 3 and part of the TNFR-Cys repeat 4. Alternative 38 amino acids at the C terminus. Missing part of TNFR-Cys repeat #4, the TM domain and the cytoplasmic domain.
5	MCD40Alt19	195	Contains 165 N-terminal amino acids, including entire TNFR-Cys repeats 1, 2, 3 and part of the TNFR-Cys repeat 4. Alternative 30 amino acids at the C terminus. Missing part of TNFR-Cys repeat #4, the TM domain and the cytoplasmic domain.
6	MCD40Alt6Corecte	211	Contains 165 N-terminal amino acids, including entire TNFR-Cys repeats 1, 2, 3 and part of the TNFR-Cys repeat 4. Insertion of 9 amino acids at the position #86 of the wild type protein (instead of the original Asn). Alternative 30 amino acids at the C terminus. Missing part of TNFR-Cys repeat #4, the TM domain and the cytoplasmic domain.

SEQ ID NOS. 1 and 2 are from human source origin.

SEQ ID NOS: 4-6 are for mouse ortholog sequence.

- 5 *"CD40R Variants products – also referred at times as the "CD40R variants proteins" or "CD40R variants polypeptides" – is an amino acid sequence encoded*

by the CD40R variants nucleic acid sequences which is a naturally occurring mRNA sequence obtained as a result of alternative splicing. The amino acid sequences may be a peptide, a protein, as well as peptides or proteins having *chemically modified* amino acids (see below) such as a glycopeptide or glycoprotein. The CD40R variants products are shown in any one of SEQ ID NO: 7 to SEQ ID NO: 12. The term also includes *homologs* (see below) of said sequences in which one or more amino acids has been added, deleted, *substituted* (see below) or *chemically modified* (see below) as well as *fragments* (see below) of this sequence having at least 10 amino acids. As indicated above, this sequence refers to the extracellular domain of the CD40R.

10

"Fragments of CD40 variants nucleic acid sequences" – a partial sequence of any one of SEQ ID NO: 1 to SEQ ID NO: 6 which includes the regions which contains the variation in nucleotides between the variant and the original sequences. These regions (in the amino acid level) are as depicted in the above Table 1.

15

"Fragments of CD40R variant product" – amino acid sequences coded by the above nucleic acid fragment, containing regions by which the variant differs from the original sequence as indicated in Table 1.

20 ***"Nucleic acid sequence"*** – a sequence composed of DNA nucleotides, RNA nucleotides or a combination of both types and may includes natural nucleotides, chemically modified nucleotides and synthetic nucleotides.

"Amino acid sequence" – a sequence composed of any one of the 20 naturally appearing amino acids, amino acids which have been *chemically modified* (see below), or composed of synthetic amino acids.

"Homologues of variants/products" – amino acid sequences of variants in which one or more amino acids has been added, deleted or replaced. The altered amino

acid shall be in regions where the variant differs from the original sequence, for example, according to the explanation in Table 1.

"Conservative substitution" - refers to the substitution of an amino acid in one class by an amino acid of the same class, where a class is defined by common physicochemical amino acid side chain properties and high substitution frequencies in homologous proteins found in nature, as determined, for example, by a standard Dayhoff frequency exchange matrix or BLOSUM matrix. Six general classes of amino acid side chains have been categorized and include:

5 class by an amino acid of the same class, where a class is defined by common
physicochemical amino acid side chain properties and high substitution
frequencies in homologous proteins found in nature, as determined, for example,
by a standard Dayhoff frequency exchange matrix or BLOSUM matrix. Six
general classes of amino acid side chains have been categorized and include:
10 Class I (Cys); Class II (Ser, Thr, Pro, Ala, Gly); Class III (Asn, Asp, Gln, Glu);
Class IV (His, Arg, Lys); Class V (Ile, Leu, Val, Met); and Class VI (Phe, Tyr,
Trp). For example, substitution of an Asp for another class III residue such as
Asn, Gln, or Glu, is a conservative substitution.

15 *"Non-conservative substitution"* - refers to the substitution of an amino acid in
one class with an amino acid from another class; for example, substitution of an
Ala, a class II residue, with a class III residue such as Asp, Asn, Glu, or Gln.

"Chemically modified" - when referring to the product of the invention, means a
20 product (protein) where at least one of its amino acid residues is modified either
by natural processes, such as processing or other post-translational modifications,
or by chemical modification techniques which are well known in the art. Among
the numerous known modifications typical, but not exclusive examples include:
acetylation, acylation, amidation, ADP-ribosylation, glycosylation, GPI anchor
25 formation, covalent attachment of a lipid or lipid derivative, methylation,
myristylation, pegylation, prenylation, phosphorylation, ubiquitination, or any
similar process.

"Biologically active" - refers to the variant product having some sort of biological activity, for example, capability of binding to the CD40 ligand (CD40-L) or to other agonists of the original CD40R as known.

5 *"Immunologically active"* defines the capability of a natural, recombinant or synthetic variant product, or any fragment thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies. Thus, for example, an immunologically active fragment of variant product denotes a fragment which retains some or all of the immunological properties of
10 the variant product, e.g can bind specific anti-variant product antibodies or which can elicit an immune response which will generate such antibodies or cause proliferation of specific immune cells which produce variant.

"Optimal alignment" - is defined as an alignment giving the highest percent
15 identity score. Such alignment can be performed using a variety of commercially available sequence analysis programs, such as the local alignment program LALIGN using a ktup of 1, default parameters and the default PAM. A preferred alignment is the one performed using the CLUSTAL-W program from MacVector (TM), operated with an open gap penalty of 10.0, an extended gap
20 penalty of 0.1, and a BLOSUM similarity matrix. If a gap needs to be inserted into a first sequence to optimally align it with a second sequence, the percent identity is calculated using only the residues that are paired with a corresponding amino acid residue (i.e., the calculation does not consider residues in the second sequences that are in the "gap" of the first sequence). In case of alignments of
25 known gene sequences with that of the new variant, the optimal alignment invariably included aligning the identical parts of both sequences together, then keeping apart and unaligned the sections of the sequences that differ one from the other.

"*Having at least 90% identity*" - with respect to two amino acid or nucleic acid sequence sequences, refers to the percentage of residues that are identical in the two sequences when the sequences are optimally aligned. Thus, 90% amino acid sequence identity means that 90% of the amino acids in two or more optimally aligned polypeptide sequences are identical.

"*Isolated nucleic acid molecule having an variant nucleic acid sequence*" - is a nucleic acid molecule that includes the CD40R variant nucleic acid coding sequence. Said isolated nucleic acid molecule may include the CD40R variant nucleic acid sequence as an independent insert; may include the CD40R variant nucleic acid sequence fused to an additional coding sequences, encoding together a fusion protein in which the variant coding sequence is the dominant coding sequence (for example, the additional coding sequence may code for a signal peptide); the CD40R variant nucleic acid sequence may be in combination with non-coding sequences, e.g., introns or control elements, such as promoter and terminator elements or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host; or may be a vector in which the CD40R variant protein coding sequence is a heterologous.

"*Expression vector*" - refers to vectors that have the ability to incorporate and express heterologous DNA fragments in a foreign cell. Many prokaryotic and eukaryotic expression vectors are known and/or commercially available. Selection of appropriate expression vectors is within the knowledge of those having skill in the art.

"*Deletion*" - is a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

"Insertion" or "addition" - is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues, respectively, as compared to the naturally occurring sequence.

- 5 *"Substitution"* - replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively. As regards amino acid sequences the substitution may be conservative or non-conservative.

10 *"Antibody"* - refers to IgG, IgM, IgD, IgA, and IgG antibody. The definition includes polyclonal antibodies or monoclonal antibodies. This term refers to whole antibodies or fragments of the antibodies comprising the antigen-binding domain of the anti-variant product antibodies, e.g. antibodies without the Fc portion, single chain antibodies, fragments consisting of essentially only the variable, antigen-binding domain of the antibody, etc.

15

"Treating a disease" - refers to administering a therapeutic substance effective to ameliorate symptoms associated with a disease, to lessen the severity or cure the disease, or to prevent the disease from occurring.

- 20 *"Detection"* - refers to a method of detection of a disease, disorder, pathological or normal condition. This term may refer to detection of a predisposition to a disease as well as for establishing the prognosis of the patient by determining the severity of the disease.

25 *"Probe"* - the CD40R variant nucleic acid sequence, or a sequence complementary therewith, when used to detect presence of other similar sequences in a sample or of sequences having some homology with this sequence. The detection is carried out by identification of hybridization complexes between the probe and the assayed sequence. The probe may be
30 attached to a solid support or to a detectable label.

“*Original CD40R*” – the amino acid or nucleic acid sequence from which the CD40R variants of the invention have been varied as a result of alternative slicing. The original nucleic sequence is the sequence of the human CD40 receptor depicted as CD40_HUMAN Swiss Prot under Accession Number P25942 and the original amino acid sequence is the sequence encoded by it.

SUMMARY OF THE INVENTION

The present invention is based on the finding of six novel, naturally occurring splice variants of the CD40 receptor (CD40R), which are naturally occurring sequences obtained by alternative splicing of the known CD40R gene depicted as CD40_HUMAN Swiss Prot under Accession Number P25942. The novel splice variants of the invention are not merely truncated forms, or fragments of the known gene, but rather novel sequences which naturally occur within the body of individuals. These novel variants in fact contain only the extracellular domains of the original CD40R.

The term “*alternative splicing*” in the context of the present invention and claims refers to: exon exclusion, and deletion of terminal sequences in the variants as compared to the original sequence.

The novel CD40R variants of the invention retains the ligand-binding (extracellular) domain of the original CD40R, and thus are capable of binding to its ligands (for example the CD40-L) and decreasing in the individual the amounts of such free ligands available for binding to the original CD40R. Thus the CD40R variants of the invention may act as a “*scavengers*” of the CD40 ligand, since they can bind those ligands without causing signal transduction due to said binding, and thus effectively lowers the amount of said ligands. Since the variants are secreted they can exert their scavenging effect even in body fluids.

The novel CD40R variants may also serve for detection purposes, i.e. their presence or level may be indicative of a disease, disorder, pathological or normal condition involving CD40 receptor such as inflammatory diseases, autoimmune

diseases involving the immune system, pathological conditions, or alternatively the ratio between the variants' level and the level of the original CD40R peptide from which they have been varied, or the ratio of any variants with respect to each other may be indicative to such a disease, disorder, pathological or normal condition.

5 For example, for detectional purposes, it is possible to establish differential expression of the CD40R variants in various tissues as compared to the original CD40R. The variants (either each separately or both) may be expressed mainly in one tissue, while the original CD40R sequence from which they have been varied, may be expressed mainly in another tissue. Understanding of the distribution of the
10 variants as compared to the original sequence or as compared to one another in various tissues may be helpful in basic research, for understanding the physiological function of the gene as well as may help in targeting pharmaceuticals or developing pharmaceuticals.

The detection may be by determination of the presence or the level of expression
15 of the CD40R variants within a specific cell population, comparing said presence or level between various cell types in a tissue, between different tissues and between individuals.

Thus the present invention provides by its first aspect, a novel isolated nucleic acid molecule comprising or consisting of the sequence of any one of SEQ ID NO: 1
20 to SEQ ID NO: 6, fragments of said coding sequence having at least 20 nucleic acids or a molecule comprising a sequence having at least 90% identity to SEQ ID NO:1 to SEQ ID NO: 6.

The present invention further provides a protein or polypeptide comprising or consisting of an amino acid sequence encoded by any of the above nucleic acid
25 sequences, termed herein "*CD40R variant product*", for example, an amino acid sequence having the sequence as depicted in any one of SEQ ID NO:7 to SEQ ID NO:12, fragments of the above amino acid sequence having a length of at least 10 amino acids coded by the above fragments of the nucleic acid, as well as homologues of the above amino acid sequences in which one or more of the amino acid residues

has been substituted (by conservative or non-conservative substitution) added, deleted, or chemically modified.

The present invention further provides nucleic acid molecule comprising or consisting of a sequence which encodes the above amino acid sequences, (including the fragments and homologues of the amino acid sequences). Due to the degenerative nature of the genetic code, a plurality of alternative nucleic acid sequences, beyond the one depicted by any one of SEQ ID NO:1 to SEQ ID NO:6, can code for the amino acid sequence of the invention. Those alternative nucleic acid sequence which code for the same amino acid sequences depicted any one of the sequences SEQ ID NO:7 to SEQ ID NO:12 are also an aspect of the of the present invention.

The present invention further provides expression vectors and cloning vectors comprising any of the above nucleic acid sequences, as well as host cells transfected by said vectors.

The present invention still further provides pharmaceutical compositions comprising, as an active ingredient, said nucleic acid molecules, said expression vectors, or said protein or polypeptide.

These pharmaceutical compositions are suitable for the treatment of diseases and pathological conditions, which can be ameliorated or cured by decreasing the levels of any one of the ligands of the original CD40R. By the term "*ligands*" it is meant not only the CD40-L itself, but any other compounds such as TRAF3 TRAF2 which are known to interact with the CD40 receptor. Examples of such diseases are: autoimmune diseases such as arthritis, rheumatoid arthritis, lupus, (SLE), and multiple sclerosis. The compositions may also be used to prevent development of graft versus host disease (GVHD) encountered after bone-marrow transplantations.

The CD40R product may also be used for screening or constructing pharmaceuticals with improved specificity. Targeting pharmaceuticals to specific tissues (which express one variant), or targeting them against one condition (in which a particular variant is expressed) may be aided by the variants of the invention which enable screening or constructing pharmaceuticals with improved tissue, or condition specificity.

By a second aspect, the present invention provides a nucleic acid molecule comprising or consisting of a non-coding sequence which is complementary to that of any one of SEQ ID NO:1 to SEQ ID NO:6, or complementary to a sequence having at least 90% identity to said sequences or a fragment of said sequences. The complementary sequence may be a DNA sequence which hybridizes with the sequences of SEQ ID NO:1 to SEQ ID NO:6 or hybridizes to a portion of those sequences having a length sufficient to inhibit the transcription of the complementary sequences. The complementary sequence may be a DNA sequence which can be transcribed into an mRNA being an antisense to the mRNA transcribed from SEQ ID NO:1 to SEQ ID NO:6 or into an mRNA which is an antisense to a fragment of the mRNA transcribed from SEQ ID NO:1 to SEQ ID NO:6 which has a length sufficient to hybridize with the mRNA transcribed from any one of SEQ ID NO:1 to SEQ ID NO:6, so as to inhibit its translation. The complementary sequence may also be the mRNA or the fragment of the mRNA itself.

The nucleic acids of the second aspect of the invention may be used for therapeutic or diagnostic applications for example as probes used for the detection of the CD40R variants of the invention. The presence of the CD40R variants transcripts or the level of the variants transcripts may be indicative of a multitude of diseases, disorders and various pathological as well as normal conditions. In addition, the ratio of the level of the transcripts of the variants of the invention may also be compared to that of the transcripts of the original CD40R sequences from which they have been varied or the ratio of each other, and said ratio may be indicative to a multitude of diseases, disorders and various pathological and normal conditions. Comparison may be aided by the fact that while the known CD40 receptor has both cytoplasmic and extracellular regions the variants of the invention have essentially only extracellular regions and are thus secreted soluble.

The present invention also provides expression vectors comprising any one of the above defined complementary nucleic acid sequences and host cells transfected with said nucleic acid sequences or vectors, being complementary to those specified in the first aspect of the invention.

The invention also provides anti-variant product antibodies, namely antibodies directed against the CD40R variants products which specifically bind to said CD40R variants products. Said antibodies are useful both for diagnostic and therapeutic purposes. For example said antibodies may be as an active ingredient in a pharmaceutical composition as will be explained below.

The present invention also provides pharmaceutical compositions comprising, as an active ingredient, the nucleic acid molecules which comprise or consist of said complementary sequences, or of a vector comprising said complementary sequences. The pharmaceutical composition thus provides pharmaceutical compositions comprising, as an active ingredient, said anti-variant product antibodies.

According to the third aspect of the invention the present invention provides methods for detecting the level of the transcripts (mRNA) of said CD40R variants product in a body fluid sample, or in a specific tissue sample, for example by use of probes comprising or consisting of said coding sequences; as well as methods for detecting levels of expression of said product in tissue, e.g. by the use of antibodies capable of specifically reacting with the CD40 variants products of the invention. Detection of the level of the expression of the CD40 variants of the invention in particular as compared to that of the original sequence from which it was varied or compared to each other may be indicative of a plurality of physiological or pathological conditions.

The method, according to this latter aspect, for detection of a nucleic acid sequence which encodes the CD40R variants products in a biological sample, comprises the steps of:

(a) providing a probe comprising at least one of the nucleic acid sequences defined above;

(b) contacting the biological sample with said probe under conditions allowing hybridization of nucleic acid sequences thereby enabling formation of hybridization complexes;

(c) detecting hybridization complexes, wherein the presence of the complex indicates the presence of nucleic acid sequence encoding the CD40R variants products in the biological sample.

The method as described above is qualitative, i.e. indicates whether the
5 transcripts are present in or absent from the sample. The method can also be quantitative, by determining the level of hybridization complexes and then calibrating said levels to determining levels of transcripts of the desired variants in the sample.

Both qualitative and quantitative determination methods can be used for diagnostic, prognostic and therapy planning purposes.

10 By a preferred embodiment the probe is part of a nucleic acid chip used for detection purposes, i.e. the probe is a part of an array of probes each present in a known location on a solid support.

The nucleic acid sequences used in the above method may be a DNA sequence an RNA sequence, etc; they may be a coding or a sequence or a sequence
15 complementary thereto (for respective detection of RNA transcripts or coding-DNA sequences). By quantization of the level of hybridization complexes and calibrating the quantified results it is possible also to detect the level of the transcripts in the sample.

Methods for detecting mutations in the region coding for the CD40R variants
20 products are also provided, which may be methods carried-out in a binary fashion, namely merely detecting whether there is any mismatches between the normal variant nucleic acid sequence of the invention and the one present in the sample, or carried-out by specifically detecting the nature and location of the mutation.

The present invention also concerns a method for detecting the CD40R
25 variants products in a biological sample, comprising the steps of:

(a) contacting with said biological sample the antibody of the invention, thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the
30 presence of the CD40R variants products in said biological sample.

As indicated above, the method can be quantitized to determine the level or the amount of the CD40R variants in the sample, alone or in comparison to the level of the original CD40R amino acid sequence from which it was varied, and qualitative and quantitative results may be used for diagnostic, prognostic and therapy planning purposes.

BRIEF DESCRIPTION OF THE DRAWING

Fig. 1 shows multiple alignment of four amino acid sequences ID NOS: 3-6 of mouse origin (depicted in SEQ ID NO:9 to SEQ ID NO:12 to each other and to the original sequence;

Fig. 2 shows Western blot analysis (top) of St-9 cells infected with CD40 expression vectors and an abnormal spectrum at 280 nm as a function of time;

Fig. 3 shows Western blot analysis of CD40 secreted from St-0 cells transfected with an expression vector;

Fig. 4 shows comparison by alignment of the original CD40R nucleic acid sequence as obtained from Swiss Prot Accession No. 25942 and SEQ ID NO:1;

Fig. 5 shows a comparison of the original CD40 nucleic acid sequence and SEQ ID NO:2; and

Fig. 6 shows comparison by alignment of the original CD40R amino acid sequence and SEQ ID NO:7.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Example I: CD40R variants nucleic acid sequence

The nucleic acid sequences of the invention include nucleic acid sequences which encode CD40R variants products and fragments and analogs thereof. The nucleic acid sequences may alternatively be sequences complementary to the above coding sequences, or to regions of said coding sequence. The length of the complementary sequences is sufficient to avoid the expression of the coding sequence. The nucleic acid sequences may be in the form of RNA or in the form of DNA, and include messenger RNA, synthetic

RNA and DNA, cDNA, and genomic DNA. The DNA may be double-stranded or single-stranded, and if single-stranded may be the coding strand or the non-coding (anti-sense, complementary) strand. The nucleic acid sequences may also both include dNTPs, rNTPs as well as non naturally occurring sequences.

5 The sequence may also be a part of a hybrid between an amino acid sequence and a nucleic acid sequence.

In a general embodiment, the nucleic acid sequence has at least 90% identity with any one of the sequence identified as SEQ ID NO:1 to SEQ ID NO:6.

10 The nucleic acid sequences may include the coding sequence by itself. By another alternative the coding region may be in combination with additional coding sequences, such as those coding for fusion protein or signal peptides, in combination with non-coding sequences, such as introns and control elements, promoter and terminator elements or 5' and/or 3' untranslated regions, effective

15 for expression of the coding sequence in a suitable host, and/or in a vector or host environment in which the variant nucleic acid sequences is introduced as a heterologous sequence.

The nucleic acid sequences of the present invention may also have the CD40R variants products coding sequences fused in-frame to a marker sequence

20 which allows for purification of the variant product. The marker sequence may be, for example, a hexahistidine tag to provide for purification of the mature polypeptide fused to the marker in the case of a bacterial host, or, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza

25 hemagglutinin protein (Wilson, I., *et al. Cell* 37:767 (1984)).

Also included in the scope of the invention are fragments as defined above also referred to herein as oligonucleotides, typically having at least 20 bases, preferably 20-30 bases corresponding to a region of the coding-sequence nucleic acid sequence. The fragments may be used as probes, primers, and when

complementary also as antisense agents, and the like, according to known methods.

As indicated above, the nucleic acid sequence may be substantially a depicted in SEQ ID NO:1 to SEQ ID NO:6 or fragments thereof or sequences
5 having at least 90% identity to the above sequence as explained above. Alternatively, due to the degenerative nature of the genetic code, the sequence may be a sequence coding for any one of the amino acid sequence of SEQ ID NO:7 or SEQ ID NO:12, or fragments or analogs of said amino acid sequence.

10 A. Preparation of nucleic acid sequences

The nucleic acid sequences may be obtained by screening cDNA libraries using oligonucleotide probes which can hybridize to or PCR-amplify nucleic acid sequences which encode the CD40R variants products disclosed above. cDNA
libraries prepared from a variety of tissues are commercially available and
15 procedures for screening and isolating cDNA clones are well-known to those of skill in the art. Such techniques are described in, for example, Sambrook *et al.* (1989) Molecular Cloning: A Laboratory Manual (2nd Edition), Cold Spring Harbor Press, Plainview, N.Y. and Ausubel FM *et al.* (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.

20 The nucleic acid sequences may be extended to obtain upstream and downstream sequences such as promoters, regulatory elements, and 5' and 3' untranslated regions (UTRs). Extension of the available transcript sequence may be performed by numerous methods known to those of skill in the art, such as PCR or primer extension (Sambrook *et al.*, *supra*), or by the RACE method
25 using, for example, the Marathon RACE kit (Clontech, Cat. # K1802-1).

Alternatively, the technique of "restriction-site" PCR (Gobinda *et al.* *PCR Methods Applic.* 2:318-22, (1993)), which uses universal primers to retrieve flanking sequence adjacent a known locus, may be employed. First, genomic DNA is amplified in the presence of primer to a linker sequence and a primer
30 specific to the known region. The amplified sequences are subjected to a second

round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR can be used to amplify or extend sequences using divergent
5 primers based on a known region (Triglia, T. *et al.*, *Nucleic Acids Res.* **16**:8186, (1988)). The primers may be designed using OLIGO(R) 4.06 Primer Analysis Software (1992: National Biosciences Inc, Plymouth, Minn.), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72°C.
10 The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Capture PCR (Lagerstrom, M. *et al.*, *PCR Methods Applic.* **1**:111-19, (1991)) is a method for PCR amplification of DNA fragments adjacent to a
15 known sequence in human and yeast artificial chromosome DNA. Capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered double-stranded sequence into a flanking part of the DNA molecule before PCR.

Another method which may be used to retrieve flanking sequences is that
20 of Parker, J.D., *et al.*, *Nucleic Acids Res.*, **19**:3055-60, (1991)). Additionally, one can use PCR, nested primers and PromoterFinder™ libraries to "walk in" genomic DNA (PromoterFinder™; Clontech, Palo Alto, CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions. Preferred libraries for screening for full length cDNAs are ones that have been
25 size-selected to include larger cDNAs. Also, random primed libraries are preferred in that they will contain more sequences which contain the 5' and upstream regions of genes.

A randomly primed library may be particularly useful if an oligo d(T) library does not yield a full-length cDNA. Genomic libraries are useful for
30 extension into the 5' nontranslated regulatory region.

The nucleic acid sequences and oligonucleotides of the invention can also be prepared by solid-phase methods, according to known synthetic methods. Typically, fragments of up to about 100 bases are individually synthesized, then joined to form continuous sequences up to several hundred bases.

5

B. Use of CD40R variants nucleic acid sequences for the production of CD40R variants products

In accordance with the present invention, nucleic acid sequences specified
10 above may be used as recombinant DNA molecules that direct the expression of CD40R variant products.

As will be understood by those of skill in the art, it may be advantageous to produce CD40R variants product-encoding nucleotide sequences possessing codons other than those which appear in SEQ ID NO:1 to SEQ ID NO:6 which
15 are those which naturally occur in the human genome. Codons preferred by a particular prokaryotic or eukaryotic host (Murray, E. *et al. Nuc Acids Res.*, 17:477-508, (1989)) can be selected, for example, to increase the rate of variant product expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than transcripts produced from naturally
20 occurring sequence.

The nucleic acid sequences of the present invention can be engineered in order to alter a CD40R variants products coding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the product. For example, alterations may be
25 introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, etc.

The present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs
30 comprise a vector, such as a plasmid or viral vector, into which nucleic acid sequences of the invention have been inserted, in a forward or reverse

orientation. In a preferred aspect of this embodiment, the constructs further comprise regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. Appropriate
5 cloning and expression vectors for use with prokaryotic and eukaryotic hosts are also described in Sambrook, *et al.*, (*supra*).

The present invention also relates to host cells which are genetically engineered with vectors of the invention, and the production of the product of the invention by recombinant techniques. Host cells are genetically engineered (i.e.,
10 transduced, transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the
15 expression of the variant nucleic acid sequence. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art.

The nucleic acid sequences of the present invention may be included in any one of a variety of expression vectors for expressing a product. Such vectors
20 include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.
25 The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and related sub-cloning procedures are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate transcription control sequence (promoter) to direct mRNA synthesis. Examples of such promoters include: LTR or SV40 promoter, the *E.coli lac* or *trp* promoter, the phage lambda *P_L* promoter, and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vectors also contains a ribosome binding site for translation initiation, and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E.coli*.

The vectors containing the appropriate DNA sequence as described above, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein. Examples of appropriate expression hosts include: bacterial cells, such as *E.coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* and *Spodoptera Sf9*; animal cells such as CHO, COS, HEK 293 or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein. The invention is not limited by the host cells employed.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the CD40R variant product. For example, when large quantities of CD40R variant product are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be desirable. Such vectors include, but are not limited to, multifunctional *E.coli* cloning and expression vectors such as *Bluescript*(R) (Stratagene), in which the CD40R variants polypeptides coding sequence may be ligated into the vector in-frame with sequences for the amino-terminal Met and the subsequent 7 residues of beta-galactosidase so that a hybrid protein is

produced: *pIN* vectors (Van Heeke & Schuster *J. Biol. Chem.* **264**:5503-5509, (1989)); *pET* vectors (Novagen, Madison WI); and the like.

In the yeast *Saccharomyces cerevisiae* a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase and
5 PGH may be used. For reviews, see Ausubel *et al.* (*supra*) and Grant *et al.*, (*Methods in Enzymology* **153**:516-544, (1987)).

In cases where plant expression vectors are used, the expression of a sequence encoding variant products may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of
10 *CaMV* (Brisson *et al.*, *Nature* **310**:511-514, (1984)) may be used alone or in combination with the omega leader sequence from TMV (Takamatsu *et al.*, *EMBO J.*, **6**:307-311, (1987)). Alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi *et al.*, *EMBO J.* **3**:1671-1680, (1984); Broglie *et al.*, *Science* **224**:838-843, (1984)); or heat shock promoters (Winter J and
15 Sinibaldi R.M., *Results Probl. Cell Differ.*, **17**:85-105, (1991)) may be used. These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. For reviews of such techniques, see Hobbs S. or Murry L.E. (1992) in McGraw Hill Yearbook of Science and Technology, McGraw Hill, New York, N.Y., pp 191-196; or Weissbach and Weissbach
20 (1988) *Methods for Plant Molecular Biology*, Academic Press, New York, N.Y., pp 421-463.

CD40R variants products may also be expressed in an insect system. In one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in
25 *Trichoplusia* larvae. The CD40R variants products coding sequence may be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of CD40R variants coding sequences will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein coat. The recombinant viruses are then
30 used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which variant protein

is expressed (Smith *et al.*, *J. Virol.* 46:584, (1983); Engelhard, E.K. *et al.*, *Proc. Natl. Acad. Sci.* 91:3224-7, (1994)).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, CD40R variants products coding sequences may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a nonessential E1 or E3 region of the viral genome will result in a viable virus capable of expressing variant protein in infected host cells (Logan and Shenk, *Proc. Natl. Acad. Sci.* 81:3655-59, (1984). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be required for efficient translation of variants products coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where CD40R variants products coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon must be provided. Furthermore, the initiation codon must be in the correct reading frame to ensure transcription of the entire insert. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (Scharf, D. *et al.*, (1994) *Results Probl. Cell Differ.*, 20:125-62, (1994); Bittner *et al.*, *Methods in Enzymol* 153:516-544, (1987)).

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium

phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, L., Dibner, M., and Battey, L. (1986) Basic Methods in Molecular Biology). Cell-free translation systems can also be employed to produce polypeptides using RNAs derived from the DNA constructs of the present invention.

A host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the protein include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing which cleaves a "pre-pro" form of the protein may also be important for correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, 293, WI38, etc. have specific cellular machinery and characteristic mechanisms for such post-translational activities and may be chosen to ensure the correct modification and processing of the introduced, foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express variant products may be transformed using expression vectors which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clumps of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler M., *et al.*, *Cell* 11:223-32, (1977)) and adenine phosphoribosyltransferase (Lowy L., *et al.*, *Cell* 22:817-23, (1980)) genes which can be employed in *tk*- or *aprt*- cells, respectively. Also, antimetabolite,

antibiotic or herbicide resistance can be used as the basis for selection; for example, *dhfr* which confers resistance to methotrexate (Wigler M., *et al.*, *Proc. Natl. Acad. Sci.* **77**:3567-70, (1980)); *npt*, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. *et al.*, *J. Mol. Biol.*, **150**:1-14, (1981)) and *als* or *pat*, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, *trpB*, which allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman S.C. and R.C. Mulligan, *Proc. Natl. Acad. Sci.* **85**:8047-51, (1988)). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate, GUS, and luciferase and its substrates, luciferin and ATP, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. *et al.*, *Methods Mol. Biol.*, **55**:121-131, (1995)).

Host cells transformed with nucleotide sequences encoding CD40R variants products may be cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The product produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing nucleic acid sequences encoding CD40R variants products can be designed with signal sequences which direct secretion of CD40R variants products through a prokaryotic or eukaryotic cell membrane.

The CD40R variants products may also be expressed as recombinant proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp. Seattle, Wash.).

The inclusion of a protease-cleavable polypeptide linker sequence between the purification domain and CD40R variants products is useful to facilitate purification. One such expression vector provides for expression of a fusion protein comprising a variant polypeptide fused to a polyhistidine region
5 separated by an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography, as described in Porath, *et al.*, *Protein Expression and Purification*, 3:263-281, (1992)) while the enterokinase cleavage site provides a means for isolating variant polypeptide from the fusion protein. *pGEX* vectors (Promega, Madison,
10 Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to ligand-agarose beads (e.g., glutathione-agarose in the case of GST-fusions) followed by elution in the presence of free ligand.

15 Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained
20 for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, or other methods, which are well known to those skilled in the art.

The CD40R variants products can be recovered and purified from
25 recombinant cell cultures by any of a number of methods well known in the art, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, and lectin chromatography. Protein refolding
30 steps can be used, as necessary, in completing configuration of the mature

protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

C. Use of variant to produce proteins

5 C.1 Separation:

Sf-9 cells were infected with sCD40 expressing baculovirus (Ac-sCD40) comprising the amino acid sequence of SEQ ID NO:3 at MOI of 2. The cells were grown in 28°C at continuous shaking (90rpm). At 60 hours post infection (hpi) the medium was collected and cells were separated from the medium by
10 centrifugation at 5000RPM for 5 minutes. 10ml medium was separated using cation exchange chromatography with SP-Sepharose column. The Column was equilibrated with PBS pH-6.5 and following loading of the sample on the column the column was washed with PBS to elute the unbound proteins (flow through fraction). Elution was done with increasing concentration of NaCl at flow rate of
15 2ml/min (5%NaCl/min).

The different fractions were subjected to SDS-PAGE electrophoresis and to western blotting using anti mCD40 antibody, and the results are shown in Fig. 2.

20 C.1 Secretion:

Sf-9 cells were infected with sCD40 expressing baculovirus (Ac-sCD40) at MOI of 2. The cells were grown at 28°C at continuous shaking (90rpm) and 1ml samples were collected at 24, 48 and 60 hours post infection (hpi). Following centrifugation Cells pellet was lysed with lysis buffer (50mM Tris pH
25 7.5, 1% triton X100, and protease inhibitor cocktail) at 4°C for 30 min and sonicated for 30 seconds. The sample was centrifuged for 10 minutes at 14000rpm and the sup was designated Pellet. 40 µl of the pellet preparation and of the medium (Designated Medium) were supplemented with sample buffer and electrophoreses on a 15% SDS-PAGE. Following electrophoresis the gel was
30 subjected to a semi dry protein transfer onto a nitrocellulose membrane. The

membrane was incubated with anti mCD40 antibody for 2 hours and with secondary anti rabbit antibody for an additional 1 hour.

Detection of the signal was done using a commercial western blot detection kit, and the results are shown in Fig. 3.

5

D. Diagnostic applications utilizing nucleic acid sequences

The nucleic acid sequences of the present invention may be used for a variety of diagnostic purposes. The nucleic acid sequences may be used to detect and quantitate expression of the CD40R variant in patient's cells, e.g. biopsied
10 tissues, by detecting the presence of mRNA coding for the CD40R variants products. Alternatively, the assay may be used to detect the soluble variants in the serum or blood. This assay typically involves obtaining total mRNA from the tissue or serum and contacting the mRNA with a nucleic acid probe. The probe is a nucleic acid molecule of at least 20 nucleotides, preferably 20-30
15 nucleotides, capable of specifically hybridizing with a sequence included within the sequence of a nucleic acid molecule encoding the CD40R variant product under hybridizing conditions, detecting the presence of mRNA hybridized to the probe, and thereby detecting the expression of variant. This assay can be used to distinguish between absence, presence, and excess expression of CD40R variants
20 products and to monitor levels of CD40R variants expression during therapeutic intervention. In addition, the assay may be used to compare the levels of the CD40R variant of the invention to the levels of the original CD40R sequence from which it has been varied or to levels of each other, which comparison may have some physiological meaning.

25 The invention also contemplates the use of the nucleic acid sequences as a diagnostic for diseases resulting from inherited defective variants sequences, or diseases in which the ratio of the amount of the original CD40R sequence from which the CD40R variants were varied to the novel CD40R variants of the invention is altered. These sequences can be detected by comparing the
30 sequences of the defective (i.e., mutant) CD40R variants coding region with that

of a normal coding region. Association of the sequence coding for mutant CD40R variants products with abnormal variants products activity may be verified. In addition, sequences encoding mutant CD40R variants products can be inserted into a suitable vector for expression in a functional assay system (e.g., colorimetric assay, complementation experiments in a variant protein deficient strain of HEK293 cells) as yet another means to verify or identify mutations. Once mutant genes have been identified, one can then screen populations of interest for carriers of the mutant gene.

Individuals carrying mutations in the nucleic acid sequences of the present invention may be detected at the DNA level by a variety of techniques. Nucleic acids used for diagnosis may be obtained from a patient's cells, including but not limited to such as from blood, urine, saliva, placenta, tissue biopsy and autopsy material. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR (Saiki, *et al.*, *Nature* **324**:163-166, (1986)) prior to analysis. RNA or cDNA may also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid of the present invention can be used to identify and analyze mutations in the gene of the present invention. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype.

Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA of the invention or alternatively, radiolabeled antisense DNA sequences of the invention. Sequence changes at specific locations may also be revealed by nuclease protection assays, such RNase and S1 protection or the chemical cleavage method (e.g. Cotton, *et al* *Proc. Natl. Acad. Sci. USA*, **85**:4397-4401, (1985)), or by differences in melting temperatures. "Molecular beacons" (Kostrikis L.G. *et al.*, *Science* **279**:1228-1229, (1998)), hairpin-shaped, single-stranded synthetic oligo- nucleotides containing probe sequences which are complementary to the nucleic acid of the present invention, may also be used to detect point mutations or other sequence changes as well as monitor

expression levels of variant product. Such diagnostics would be particularly useful for prenatal testing.

Another method for detecting mutations uses two DNA probes which are designed to hybridize to adjacent regions of a target, with abutting bases, where the region of known or suspected mutation(s) is at or near the abutting bases. The two probes may be joined at the abutting bases, e.g., in the presence of a ligase enzyme, but only if both probes are correctly base paired in the region of probe junction. The presence or absence of mutations is then detectable by the presence or absence of ligated probe.

Also suitable for detecting mutations in the CD40R variants products coding sequences are oligonucleotide array methods based on sequencing by hybridization (SBH), as described, for example, in U.S. Patent No. 5,547,839. In a typical method, the DNA target analyte is hybridized with an array of oligonucleotides formed on a microchip. The sequence of the target can then be "read" from the pattern of target binding to the array.

E. Therapeutic applications of nucleic acid sequences

Nucleic acid sequences of the invention may also be used for therapeutic purposes. Turning first to the second aspect of the invention (i.e. inhibition of expression of CD40R variants), expression of CD40R variants products may be modulated through antisense technology, which controls gene expression through hybridization of complementary nucleic acid sequences, i.e. antisense DNA or RNA, to the control, 5' or regulatory regions of the gene encoding variant product. For example, the 5' coding portion of the nucleic acid sequence sequence which codes for the product of the present invention is used to design an antisense oligonucleotide of from about 10 to 40 base pairs in length. Oligonucleotides derived from the transcription start site, e.g. between positions -10 and +10 from the start site, are preferred. An antisense DNA oligonucleotide is designed to be complementary to a region of the nucleic acid sequence involved in transcription (Lee *et al.*, *Nucl. Acids, Res.*, 6:3073, (1979); Cooney et

al., *Science* **241**:456, (1988); and Dervan *et al.*, *Science* **251**:1360, (1991)), thereby preventing transcription and the production of the variant products. An antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the variant products (Okano
5 *J. Neurochem.* **56**:560, (1991)). The antisense constructs can be delivered to cells by procedures known in the art such that the antisense RNA or DNA may be expressed *in vivo*. The antisense may be antisense mRNA or DNA sequence capable of coding such antisense mRNA. The antisense mRNA or the DNA coding thereof can be complementary to the full sequence of nucleic acid
10 sequences coding for the CD40R variant protein or to a fragment of such a sequence which is sufficient to inhibit production of a protein product. Antisense technologies can also be used for inhibiting expression of one variant as compared to the other, or inhibiting the expression of the variant/s as compared to the original sequence.

15 Turning now to the first aspect of the invention, i.e. expression of CD40R variants, expression of CD40R variants products may be increased by providing coding sequences for coding for said CD40R variants products under the control of suitable control elements ending its expression in the desired host.

The nucleic acid sequences of the invention may be employed in
20 combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

25 The products of the invention may also be employed in accordance with the present invention by expression of such polypeptides *in vivo*, which is often referred to as "*gene therapy*." Cells from a patient may be engineered with a nucleic acid sequence (DNA or RNA) encoding a polypeptide *ex vivo*, with the engineered cells then being provided to a patient to be treated with the
30 polypeptide. Such methods are well-known in the art. For example, cells may be

engineered by procedures known in the art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding the polypeptides of the present invention may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering products of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells *in vivo* after combination with a suitable delivery vehicle.

Retroviruses from which the retroviral plasmid vectors mentioned above may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the *PE501*, *PA317*, *psi-2*, *psi-AM*, *PA12*, *T19-14X*, *VT-19-17-H2*, *psi-CRE*, *psi-CRIP*, *GP+E-86*, *GP+envAm12*, and *DAN* cell lines as described in Miller (*Human Gene Therapy*, Vol. 1, pg. 5-14, (1990)). The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO_4 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include the nucleic acid sequence(s) encoding the polypeptides. Such retroviral vector particles then may be employed, to transduce eukaryotic cells,

either in vitro or in vivo. The transduced eukaryotic cells will express the nucleic acid sequence(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic carcinoma cells, as well as hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

The genes introduced into cells may be placed under the control of inducible promoters, such as the radiation-inducible Egr-1 promoter, (Maceri, H.J., *et al.*, *Cancer Res.*, **56**(19):4311 (1996)), to stimulate variant production or antisense inhibition in response to radiation, eg., radiation therapy for treating tumors.

Example II. CD40R Variants products

The substantially purified CD40R variant product of the invention has been defined above as the product coded from the nucleic acid sequence of the invention. Preferably the amino acid sequence is an amino acid sequence having at least 90% identity the sequence identified as SEQ ID NO:7 to SEQ ID NO:12. The protein or polypeptide may be in mature and/or modified form, also as defined above, for example, modified by cleavage of the leader sequence. Also contemplated are protein fragments having at least 10 contiguous amino acid residues, preferably at least 10-20 residues, derived from the CD40R variant products, as well as homologues as explained above.

The sequence variations are preferably those that are considered conserved substitutions, as defined above. Thus, for example, a protein with a sequence having at least 90% sequence identity with the products identified as SEQ ID NO:7 to SEQ ID NO:12, preferably by utilizing conserved substitutions as defined above is also part of the invention, and provided that it is not identical to the original peptide from which it has been varied (typically the substitutions are in regions where the variant differs from the original sequence as for example in Table 1). In a more specific embodiment, the protein has or contains the sequence identified SEQ ID NO:7 to SEQ ID NO:12. The CD40R variants

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products may be (i) one in which one or more of the amino acid residues in a sequence listed above are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue), or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the CD40R variants products is fused with another compound, such as a compound to increase the half-life of the protein (for example, polyethylene glycol (PEG)), or a moiety which serves as targeting means to direct the protein to its target tissue or target cell population (such as an antibody), or (iv) one in which additional amino acids are fused to the CD40R variant product. Such fragments, variants and derivatives are deemed to be within the scope of those skilled in the art from the teachings herein.

A. Preparation of CD40R variants products

Recombinant methods for producing and isolating the CD40R variant products, and fragments of the protein are described above.

In addition to recombinant production, fragments and portions of variant products may be produced by direct peptide synthesis using solid-phase techniques (cf. Stewart *et al.*, (1969) Solid-Phase Peptide Synthesis, WH Freeman Co. San Francisco; Merrifield J., *J. Am. Chem. Soc.*, **85**:2149-2154, (1963)). In vitro peptide synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer, Foster City, Calif.) in accordance with the instructions provided by the manufacturer. Fragments of CD40R variants products may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

B. Therapeutic uses and compositions utilizing the CD40R variants products

The CD40R variants products of the invention are generally useful in treating diseases and disorders which can be cured or ameliorated by lowering

the level of any of the CD40 ligands. Examples of such diseases are various autoimmune diseases as well as GVHD.

CD40R variant products or fragments may be administered by any of a number of routes and methods designed to provide a consistent and predictable concentration of compound at the target organ or tissue. The product-containing compositions may be administered alone or in combination with other agents, such as stabilizing compounds, and/or in combination with other pharmaceutical agents such as drugs or hormones.

CD40R variants product-containing compositions may be administered by a number of routes including, but not limited to oral, intravenous, intramuscular, transdermal, subcutaneous, topical, sublingual, or rectal means as well as by nasal application. CD40R variant product-containing compositions may also be administered via liposomes. Such administration routes and appropriate formulations are generally known to those of skill in the art.

The CD40R variants products can be given via intravenous or intraperitoneal injection. Similarly, the product may be injected to other localized regions of the body. The product may also be administered via nasal insufflation. Enteral administration is also possible. For such administration, the product should be formulated into an appropriate capsule or elixir for oral administration, or into a suppository for rectal administration.

The foregoing exemplary administration modes will likely require that the product be formulated into an appropriate carrier, including ointments, gels, suppositories. Appropriate formulations are well known to persons skilled in the art.

Dosage of the product will vary, depending upon the potency and therapeutic index of the particular polypeptide selected.

A therapeutic composition for use in the treatment method can include the product in a sterile injectable solution, the polypeptide in an oral delivery vehicle, the product in an aerosol suitable for nasal administration, or the product in a nebulized form, all prepared according to well known methods. Such

compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The product of the invention may also be used to modulate endothelial differentiation and proliferation as well as to modulate apoptosis either *ex vivo* or *in vitro*, for example, in cell cultures.

Example III. Anti-variant antibodies

A. Synthesis

In still another aspect of the invention, the purified variants products are used to produce anti-variant antibodies which have diagnostic and therapeutic uses related to the activity, distribution, and expression of the CD40R variants products.

Antibodies to the CD40R variant may be generated by methods well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, humanized, single chain, Fab fragments and fragments produced by an Fab expression library. Antibodies, i.e., those which inhibit dimer formation, are especially preferred for therapeutic use.

A fragment of the CD40R variants products for antibody induction is not required to feature biological activity but has to feature immunological activity; however, the protein fragment or oligopeptide must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids of the sequences specified in SEQ ID NO:7 to SEQ ID NO:12. Preferably they should mimic a portion of the amino acid sequence of the natural protein and may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of CD40R variants proteins amino acids may be fused with those of another protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule. Procedures well known in the art can be used for the production of antibodies to CD40R variants products.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, etc may be immunized by injection with CD40R variants products or any portion, fragment or oligopeptide which retains immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include but are not limited to Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum* are potentially useful human adjuvants.

Monoclonal antibodies to CD40R variants protein may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Koehler and Milstein (*Nature* **256**:495-497, (1975)), the human B-cell hybridoma technique (Kosbor *et al.*, *Immunol. Today* **4**:72, (1983); Cote *et al.*, *Proc. Natl. Acad. Sci.* **80**:2026-2030, (1983)) and the EBV-hybridoma technique (Cole, *et al.*, *Mol. Cell Biol.* **62**:109-120, (1984)).

Techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can also be used (Morrison *et al.*, *Proc. Natl. Acad. Sci.* **81**:6851-6855, (1984); Neuberger *et al.*, *Nature* **312**:604-608, (1984); Takeda *et al.*, *Nature* **314**:452-454, (1985)). Alternatively, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778) can be adapted to produce single-chain antibodies specific for the variant protein.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in Orlandi *et al.* (*Proc. Natl. Acad. Sci.* **86**:3833-3837, 1989)), and Winter G and Milstein C., (*Nature* **349**:293-299, (1991)).

Antibody fragments which contain specific binding sites for the CD40R variant protein may also be generated. For example, such fragments include, but are not limited to, the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse W.D. *et al.*, *Science* 256:1275-1281, (1989)).

10 **B. Diagnostic applications of antibodies**

A variety of protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the formation of complexes between the CD40R variants products and its specific antibody and the measurement of complex formation. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two noninterfering epitopes on a specific variant product is preferred, but a competitive binding assay may also be employed. These assays are described in Maddox D.E., *et al.*, (*J. Exp. Med.* **158**:1211, (1983)).

20 Antibodies which specifically bind the CD40R variant product are useful for the diagnosis of conditions or diseases characterized by expression of the novel CD40R variants of the invention (where normally it is not expressed) by over or under expression of CD40R variants as well as for detection of diseases in which the proportion between the amount of the CD40R variants of the invention and the original CD40R sequence from which it varied is altered. Alternatively, such antibodies may be used in assays to monitor patients being treated with CD40R variants products. Diagnostic assays for variants proteins include methods utilizing the antibody and a label to detect variants products in human body fluids or extracts of cells or tissues. The products and antibodies of
30 the present invention may be used with or without modification. Frequently, the

proteins and antibodies will be labeled by joining them, either covalently or noncovalently, with a reporter molecule. A wide variety of reporter molecules are known in the art.

A variety of protocols for measuring the CD40R variants products, using
5 either polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescent activated cell sorting (FACS). As noted above, a two-site, monoclonal-based immunoassay utilizing
10 monoclonal antibodies reactive to two non-interfering epitopes on CD40R variants products is preferred, but a competitive binding assay may be employed. These assays are described, among other places, in Maddox, *et al. (supra)*. Such protocols provide a basis for diagnosing altered or abnormal levels of CD40R variants products expression. Normal or standard values for CD40R variants
15 products expression are established by combining body fluids or cell extracts taken from normal subjects, preferably human, with antibodies to CD40R variants products under conditions suitable for complex formation which are well known in the art. The amount of standard complex formation may be quantified by various methods, preferably by photometric methods. Then, standard values obtained from normal samples may be compared with values obtained from
20 samples from subjects potentially affected by disease. Deviation between standard and subject values establishes the presence of disease state.

The antibody assays are useful to determine the level of CD40R variants products present in a body fluid sample, in order to determine whether it is being expressed at all, whether it is being overexpressed or underexpressed in the
25 tissue, or as an indication of how CD40R variants levels of variable products are responding to drug treatment.

C. Therapeutic uses of antibodies

In addition to their diagnostic use the antibodies may have a therapeutical
30 utility in blocking or decreasing the activity of the CD40R variant product in

pathological conditions where beneficial effect can be achieved by such a decrease.

The antibody employed is preferably a humanized monoclonal antibody, or a human Mab produced by known globulin-gene library methods. The
5 antibody is administered typically as a sterile solution by IV injection, although other parenteral routes may be suitable. Typically, the antibody is administered in an amount between about 1-15 mg/kg body weight of the subject. Treatment is continued, e.g., with dosing every 1-7 days, until a therapeutic improvement is seen.

10 Although the invention has been described with reference to specific methods and embodiments, it is appreciated that various modifications and changes may be made without departing from the invention.

CLAIMS:

1. An isolated nucleic acid sequence, of an alternative splicing variant of CD40 receptor (CD40R), selected from the group consisting of:
 - 5 (i) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to SEQ ID NO: 6;
 - (ii) nucleic acid sequences having at least 90% identity with any one of the sequences of (i); and
 - (iii) fragments of (i) or (ii) of at least 20 b.p.
- 10 2. An isolated nucleic acid sequence complementary to the nucleic acid sequence of Claim 1.
3. An amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence coded by the isolated nucleic acid sequence of Claim 1; and
 - 15 (ii) homologues of the amino acid sequences of (i) in which one or more amino acids has been added, deleted, replaced or chemically modified.
4. An amino acid sequence according to Claim 3, as depicted in any one of SEQ ID NO:7 to SEQ ID NO:12.
5. An isolated nucleic acid sequence coding for any one of the amino acid
20 sequences of Claim 3 or 4.
6. A purified antibody which binds specifically to any of the amino acid sequence of Claim 3 or 4.
7. An expression vector comprising any one of the nucleic acid sequences of Claim 1 or 5 and control elements for the expression of the nucleic acid sequence in a
25 suitable host.
8. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.
9. A host cell transfected by the expression vector of Claim 7 or 8.
- 30 10. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:

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- (i) the expression vector of Claim 7; and
 - (ii) any one of the amino acid sequences of Claim 3 or 4.
11. A pharmaceutical composition according to Claim 10, for treatment of diseases which can be ameliorated, cured or prevented by decreasing the level of at least one ligand of CD40R.
12. A pharmaceutical composition according to Claim 10, for treatment of diseases which can be ameliorated, cured or prevented by increasing the level of at least one of the CD40R variants of Claim 1.
13. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
- (i) any one of the nucleic acid sequences of Claim 2;
 - (ii) the expression vector of Claim 8; and
 - (iii) the purified antibody of Claim 6.
14. A pharmaceutical composition according to Claim 13, for treatment of diseases which can be ameliorated, cured or prevented by reducing the level of at least one of the CD40R variants of Claim 1.
15. A method for detecting the presence of at least one variant nucleic acid sequence of CD40R in a biological sample, comprising the steps of:
- (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and
 - (b) detecting said hybridization complex;
- wherein the presence of said hybridization complex correlates with the presence of at least one variant nucleic acid sequence in the said biological sample.
16. A method for determining the level of variant nucleic acid sequences of CD40R in a biological sample comprising the steps of:
- (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and
 - (b) determining the amount of hybridization complexes and normalizing said amount to provide the level of the at least one variant nucleic acid sequences in the sample.

17. A method for determining the ratio between the level of the nucleic acid sequence of a CD40R variant in a first biological sample and the level of the original CD40R sequence from which the variant has been varied by alternative splicing, in a second biological sample comprising:
- 5 (a) determining the level of the CD40R variant nucleic acid sequence in the first biological sample according to the method of Claim 16;
 - (b) determining the level of the CD40R original sequence in the second biological sample; and
 - (c) comprising the levels obtained in (a) and (b) to give said ratio.
- 10 18. A method according to Claim 17, wherein said first and said second biological samples are the same sample.
19. A method according to any of Claims 15 to 18, wherein the nucleic acid material of said biological sample are mRNA transcripts.
20. A method according to Claim 19, where the nucleic acid sequence is present in
- 15 a nucleic acid chip.
21. A method for identifying candidate compounds capable of binding to the amino acid sequence of Claim 3 or 4 and affecting the binding affinity of said sequences to at least one ligand of CD40, the method comprising:
- (i) providing any one of the amino acid sequences as defined in Claim 3
 - 20 or 4;
 - (ii) contacting a candidate compound with said amino acid sequence in the presence of at least one ligand of CD40;
 - (iii) determining the effect of said candidate compound on the binding of said amino acid to said ligand and selecting those compounds which show a
 - 25 significant effect on said binding.
22. A method for detecting any one of the amino acid sequences of Claim 3 or 4 in a biological sample, comprising the steps of:
- (a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and
 - 30 (b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.

23. A method for detecting the level of the amino acid sequence of any one of Claim 3 or 4 in a biological sample, comprising the steps of:

5 (a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and

 (b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

10 **24.** A method for determining the ratio between the level of any one of the amino acid sequences of Claims 3 or 4 of variant CD40R present in a first biological sample and the level of the original CD40R amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

15 (a) determining the level of the amino acid sequences of Claims 3 or 4 into a first sample by the method of Claim 23;

 (b) determining the level of the original CD40R amino acid sequence in the second sample; and

 (d) comparing the level obtained in (a) and (b) to give said ratio.

20 **25.** A method according to Claim 21, wherein said first and said second biological samples are the same sample.

mCD40Alt19	1	MVSLPRLCAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	50
mCD40Alt8		MVSLPRLCAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40Alt6Corrected		MVSLPRLCAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40-wt		MVSLPRLCAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mcd40-pFB1-1-5		MVSLPRLCAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40Alt19	51	CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	100
mCD40Alt8		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mCD40Alt6Corrected		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEPSAWGC	LGRDQGLRVK	
mCD40-wt		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mcd40-pFB1-1-5		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mCD40Alt19	101	KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	150
mCD40Alt8		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mCD40Alt6Corrected		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mCD40-wt		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mcd40-pFB1-1-5		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMAVRIRTWR	

Fig. 1

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Fig. 1 (Cont.)

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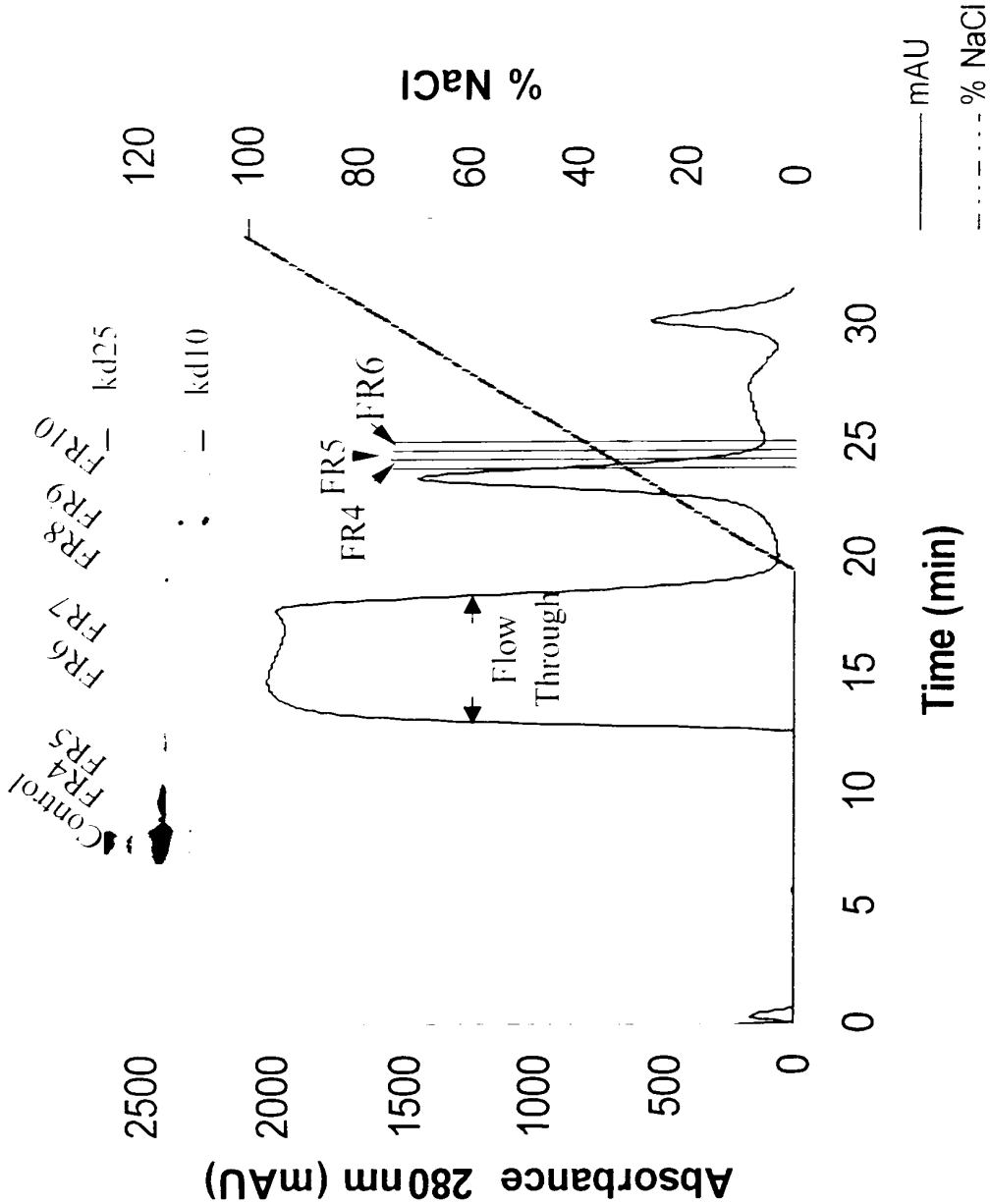


FIG.2

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Expression of sCD40 in the Baculovirus System

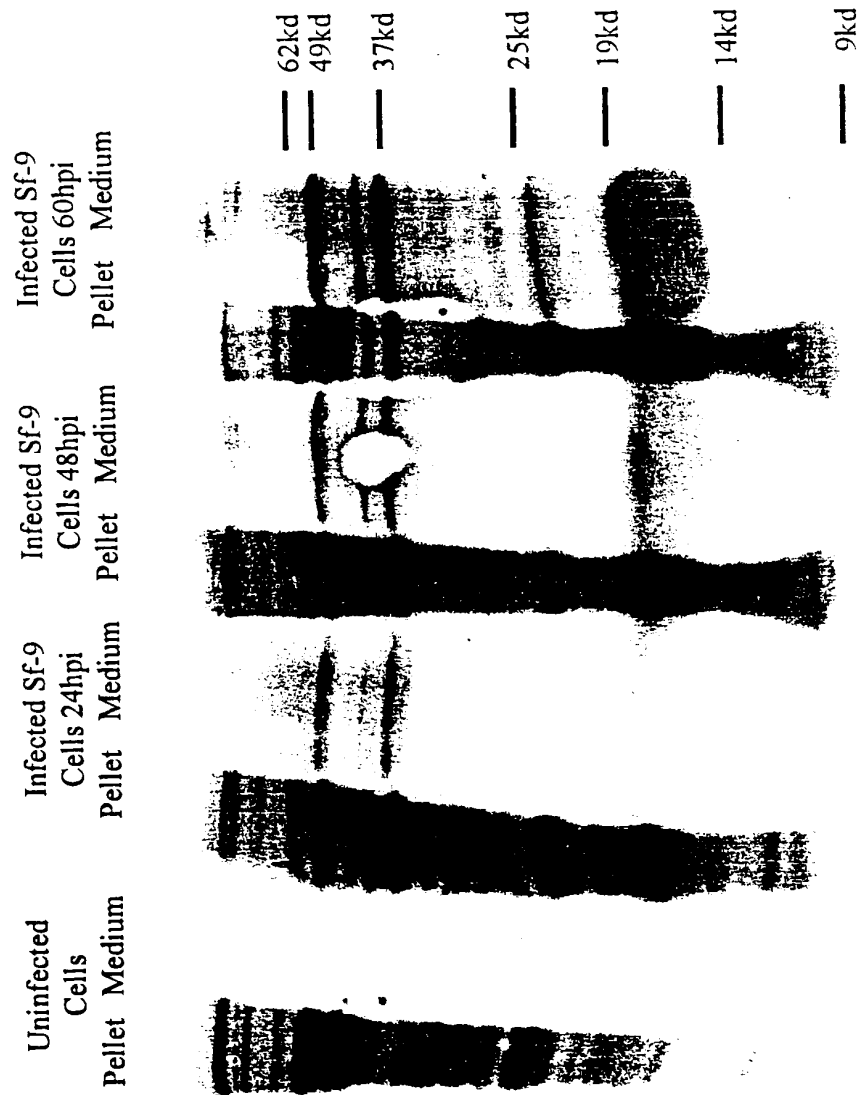


Fig. 3

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```
1 .....ATG 3
   |||
1 gcctcgctcgggcccagtggtcctgccgcctggtctcacctcgccatg 5
4 GTTCGTCGCCCTCTGCAGTGCGTCCTCTGGGGCTGCTTGCTGACCGCTGT 53
   |||||||||||||||||||||||||||||||||||||||
51 gttcgtctgcctctgcagtcggtcctctgggctgcttgctgaccgctgt 100
   . . . . .
54 CCATCCAGAACCCACTGCAATGCAGAGAAAAACAGTACCTAATAACA 103
   |||||||||||||||||||||||||||||||||||||||
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   . . . . .
104 GTCAGTGCTGTTCTTGTGCCAGCCAGCACAGAAACTGGTGAGTGACTGC 153
   |||||||||||||||||||||||||||||||||||||||
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   . . . . .
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   |||||||||||||||||||||||||||||||||||||||
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   . . . . .
204 AGACACCTGGAAACAGAGAGACACACTGCCACCCAGCACAAATACTGCGACC 253
   |||||||||||||||||||||||||||||||||||||||
251 agacacctggaacagagagacacactgccaccagcacaataactgcgacc 300
```

Fig.4

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254 CCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCAGAAACAGACACC 303
|||||
301 ccaacctagggcttcgggtccagcagaaggccacctcagaaacagacacc 350
304 ATCTGCACCTGTGAAGAAGCTGGCACTGTACGAGTGAGGCCCTGTGAGAG 353
|||||
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354 CTGTGTCCCTGCACCGCTCATGTCTGCCCGGCTTTGGGGTCAAGCAGATT. 402
|||||
401 ctgtgtcctgcaccgctcatgtctgcccggtttggggtcaagcagattg 450
403GCTGTGA 409
|||||
501 tccaatgtgtcatctgcttctcgaaaaatgtcaccccttggacaagctgtga 550
410 GACCAAAGACCTGGTTGTGCAACAGGCAGGCACAAACAAGACTGATGTTG 459
|||||
551 gaccaaaagacctggttgtgcaacaggcaggcacaacaagactgatgttg 600
460 TCTGTGTCCCCAGGATCGGCTGAGAGCCCCTGGTGGtGATCCCCCATCATC 509
|||||
601 tctgtggtccccaggatcgggtgagagccctgggtggtgatcccccatcatc 650

Fig.4(Cont.)

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510 TTCGGGATCCTGTTGC..... 526
|||||
651 ttcgggatacctgtttgccatcctcttggctgctggtcttatacaaaaaggt 700

Fig.4(Cont.)

64 CCCGGGATGGTTCTGCCTCTGCAGTCCCTCTGGGGCTGCTTGCT 113
| | |||||
42 ctcgccatggttcgtctgcctctgcagtgcgtcctctggggtgcttgct 91

114 GACCGCTGTCCATCCAGAACCACCACTGCATGCAGAGAAAACAGtACC 163
|||||
92 gaccgctgtccatccagaaccacccactgcatgcagagaaaaaacagtacc 141

164 TAATAAACAGTCAGTGCTGTTCTTTGTGCCAGCCAGGACAGAAACTGGTG 213
|||||
142 taataaacagtcagtgctgtttcttgtgccaggcacagaaaactgggtg 191

214 AGTGACTGCACAGAGTTCAC TGAAACGGAATGCCTTCCTTGCGGTGAAAG 263
|||||
192 agtgactgcacagagttcactgaaacgggaatgccttccttgcggtgaaag 241

264 CGAATTCTTAGACACCTGGAAACAGAGAGACACACTGCCACCAGCACAAAT 313
|||||
242 cgaattccttagacacacctggaacagagagacacactgccaccagcacaat 291

Fig. 5

314 ACTGCGACCCCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCagAA 363
 |||||
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 364 ACAGACACCATCTGCACCTGTGAAGAAGGCTGGCACTGTACGAGTGAGGC 413
 |||||
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 |||||
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 521 CTGATGTTGTCTGTGGTCCCCAAGATCGGCTGAGAGCCCTGGTGGTGATC 570
 |||||
 592 ctgatgttctgtggtccccaggatcgggtgagagccctggtggtgattc 641

Fig. 5 (Cont.¹)

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571 CCCATCATCTTCGGGATCCCTGTTTGCCATCCTCTTGGTGCTGGTCTTAT 620
|||||
642 cccatcatctcgggatacctgttttgccatcctcttggctggtccttat 691
.
621 CAAAAGGTGGCCAAGAAGCCAACCAATAAGGCCCCCCACCCCAAGCAGG 670
|||||
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.
671 AACCCAGGAGATCAATTTTCCCGACGATCTTCCTGGCTCCAACACTGCT 720
|||||
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.
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|||||
792 gctccagtgcaaggagactttacatggatgccaaaccggtcacccaggagga 841
.
771 TGGCAAAGAGAGTCGCATCTCAGTGCAGGAGAGACAGTGAGGCTGCCACC 820
|||||
842 tggcaaaagagagtcgcatactcagtgcaaggagagacagtgaggctgcacc 891
.

Fig. 5 (Cont.²)

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```
      .      .      .  
821 ACCCAGGAGTGTGGCCACGTGGGCAAACAGGCAGTTGGCCAGAGAGCCCTG 870  
      |||||  
892 acccaggagtgtggccacgtgggcaaacaggcagttggccagagagagcctg 941  
      .  
      871 GTGCTGCTGCTGCTGTGGCG 890  
      |||||  
      942 gtgctgctgctgcaggggtg 961
```

Fig. 5 (Cont.³)

```

1  MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSCCCLCQPGQKLVSD 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSCCCLCQPGQKLVSD 50

51 CTEFTETEC L P C G E S E F L D T W N R E T H C H Q H K Y C D P N L G L R V Q Q K G T S E T D 100
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1101 T I C T C E E G W H C T S E A C E S C V L H R S C S P G F G V K Q I A T G V S D T I C 143
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1101 T I C T C E E G W H C T S E A C E S C V L H R S C S P G F G V K Q I A V R P K T W L C 143

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Fig. 6

SEQUENCE LISTING

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<130> 1266907-COMPUGEN

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<141>

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 526

<212> DNA

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Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
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Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
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Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
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Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
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Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
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Phe Gly Val Lys Gln Ile Ala Val Arg Pro Lys Thr Trp Leu Cys Asn
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Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
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Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
 115 120 125

Phe Gly Val Lys Gln Ile Ala Cys Glu Thr Lys Asp Leu Val Val Gln
 130 135 140

Gln Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg
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Leu Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala
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Ile Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr
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Asn Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro
 195 200 205

Asp Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu
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Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
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Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
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Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
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His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
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Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
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Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
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Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160

Cys Tyr Pro Trp Thr Arg Phe Lys Val Pro Asp Ala Ser Pro Ala Gly
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 Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60
 Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80
 Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95
 Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110
 Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125
 Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
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 Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160
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 50 55 60
 Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
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 Arg His Cys Glu Pro Ser Ala Trp Gly Cys Leu Gly Arg Asp Gln Gly
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 100 105 110
 Cys Lys Glu Gly Gln His Cys Thr Ser Lys Asp Cys Glu Ala Cys Ala
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 165 170 175
 Val Pro Asp Ala Ser Pro Ala Gly His Ser Cys Arg Asp Gly His Pro
 180 185 190
 His His His Phe Arg Gly Val Ser Leu Tyr Gln Lys Gly Gly Gln Glu
 195 200 205
 Thr Lys Gly
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/IL 00/00427

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C07K16/28 A61K38/17 A61K39/395
A61K48/00 C12Q1/68 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, STRAND, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! EMBL; ID HS884118; AC R49884, 24 May 1995 (1995-05-24) HILLIER L ETAL: "CD40L receptor precursor" XP002155584 EST nucleotide sequence ---	2,7,8
X	DATABASE EMBL 'Online! EMBL; ID AI784157; AC AI784157, 2 July 1999 (1999-07-02) NATIONAL CANCER INSTITUTE, CANCER GENOM ANATOMY PROJECT (CGAP): "CD40L receptor precursor" XP002155585 EST nucleotide sequence ---	2,7,8

-/--



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

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E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

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P document published prior to the international filing date but later than the priority date claimed

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X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search

15 December 2000

Date of mailing of the international search report

28/12/2000

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/IL 00/00427

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! EMBL; ID HSH94398; AC H94398, 6 December 1995 (1995-12-06) HILLIER L ET AL: "CD40L receptor precursor" XP002155586 EST nucleotide sequence ----</p>	1,7,8
X	<p>DATABASE GCG_GENESQ:D 'Online! GCG; ID V64740; AC V64740, 29 January 1999 (1999-01-29) CAPON D ET AL: "Human immunodeficiency virus" XP002155587 HIV anti-viral oligonucleotide primer ----</p>	2,7,8
X	<p>DATABASE EMBL 'Online! EMBL; ID MMA60117; AC AA060117, 24 September 1996 (1996-09-24) MARRA M ET AL: "Mouse murine CD40 mRNA" XP002155588 EST nucleotide sequence ----</p>	1,7,8
X	<p>EP 0 555 880 A (DARTMOUTH COLLEGE ;GEN HOSPITAL CORP (US); SQUIBB BRISTOL MYERS CO) 18 August 1993 (1993-08-18) column 7 -column 9; figure 8A column 18 -column 19 ----</p>	1,3,5-9, 22
X	<p>WO 98 53842 A (UNIV PENNSYLVANIA) 3 December 1998 (1998-12-03) figure 1 ----</p>	3
X	<p>WO 97 23614 A (AMGEN INC ;LACEY DAVID L (US); BOYLE WILLIAM J (US); CALZONE FRANK) 3 July 1997 (1997-07-03) figure 2D figure 2E SEQ ID NO 132 -----</p>	3

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IL 00/00427

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
EP 0555880	A	18-08-1993	AU 3298893 A	19-08-1993
			AU 701306 B	28-01-1999
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			EP 1011704 A	28-06-2000
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			HU 9801122 A	28-08-1998
			JP 11503616 T	30-03-1999
			NO 973699 A	21-10-1997
			NZ 326579 A	28-01-1999
			PL 321938 A	05-01-1998
			SK 110797 A	12-07-1999
			TR 970550 A	21-07-1997
			US 6015938 A	18-01-2000

WO 01/05967 A1



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INTERNATIONAL COOPERATION TREATY

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NOTIFICATION OF ELECTION

(PCT Rule 61.2)

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in its capacity as elected Office

Date of mailing (day/month/year) 04 April 2001 (04.04.01)	
International application No. PCT/IL00/00427	Applicant's or agent's file reference 126690.7 DAB
International filing date (day/month/year) 19 July 2000 (19.07.00)	Priority date (day/month/year) 20 July 1999 (20.07.99)
Applicant SAVITZKY, Kinneret et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:
18 February 2001 (18.02.01)

☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was

☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

<p>The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland</p> <p>Facsimile No.: (41-22) 740.14.35</p>	<p>Authorized officer</p> <p>Charlotte ENGER</p> <p>Telephone No.: (41-22) 338.83.38</p>
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